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### AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application.

#### Listing of Claims

1. (Currently Amended) A composition comprising a protein in crystalline form wherein the protein consists of SEQ ID NO:3, wherein said protein forms a complex with an ATP-binding site ligand, and wherein the protein crystal has a crystal lattice in a P3<sub>2</sub>1 space group and unit cell dimensions, +/- 5%, of a = 72.12 Å, b = 72.12 Å and c = 241.62 Å.
2. (Currently Amended) A composition according to claim 1 wherein the protein is present in the protein crystal as a dimeric crystal unit cell comprises two protein complexes.
3. (Canceled)
4. (Previously Presented) A composition according to claim 1 wherein the crystal diffracts X-rays for a determination of structure coordinates to a resolution higher than 3.0 Angstroms.
- 5-8. (Canceled)
9. (Currently Amended) A method comprising:  
forming a crystallization volume comprising a precipitant solution and a protein that consists of SEQ ID NO:3, wherein said protein forms a complex with an ATP-binding site ligand, and wherein the protein crystal has a crystal lattice in a P3<sub>2</sub>1 space group and unit cell dimensions, +/- 5%, of a = 72.12 Å, b = 72.12 Å and c = 241.62 Å; and  
forming a crystalline form of the protein in the crystallization volume storing the crystallization volume under conditions suitable for crystal formation of the protein.
10. (Currently Amended) A method according to claim 9 wherein the protein is present in the protein crystal as a dimeric crystal unit cell comprises two protein complexes.
11. (Canceled)
12. (Previously Presented) A method according to claim 9 wherein the crystal diffracts X-rays for a determination of structure coordinates to a resolution higher than 3.0 Angstroms.

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13-14. (Canceled)

15. (Previously Presented) A method according to claim 9, the method further comprising:  
diffracting the protein crystal to produce a diffraction pattern; and  
solving the structure of the protein from the diffraction pattern.

16. (Canceled)

17. (Previously Presented) A soluble protein consisting of SEQ ID NO:3.

18-25 (Canceled)

26. (Withdrawn) A method according to claim 15, the method further comprising:  
performing rational drug design using the solved structure; and  
identifying an entity that associates with the protein.

27. (Withdrawn- Currently Amended) A method according to claim 26 wherein the protein is  
~~present in the protein crystal as a dimeric crystal unit cell comprises two protein complexes.~~

28-29. (Canceled).

30. (Withdrawn) A method according to claim 26, the method further comprising:  
selecting one or more entities based on the rational drug design; and  
contacting the selected entities with the protein.

31. (Withdrawn) A method according to claim 26, the method further comprising measuring an  
activity of the protein when contacted with the one or more entities.

32. (Withdrawn- Currently Amended) A method according to claim 26, the method further  
comprising:  
comparing activity of the protein in a presence of and in the absence of the one or more entities;  
and  
selecting entities where activity of the protein changes depending whether a particular entity is

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present.

33. (Withdrawn) A method according to claim 26, the method further comprising:  
contacting cells expressing the protein with the one or more entities; and  
detecting a change in a phenotype of the cells when a particular entity is present.
34. (Previously Presented) An isolated soluble protein consisting of residues 596-900 of SEQ ID NO:1.
35. (Currently Amended) A composition comprising a protein in crystalline form wherein the protein ~~e~~onists comprises residues 596-900 of SEQ ID NO:1, wherein said protein forms a complex with an ATP-binding site ligand, and wherein the protein crystal has a crystal lattice in a P3<sub>2</sub>1 space group and unit cell dimensions, +/- 5%, of a = 72.12Å, b = 72.12Å and c = 241.62Å.
36. (Currently Amended) A method comprising:  
forming a crystallization volume comprising a precipitant solution and a protein that ~~e~~onists comprises residues 596-900 of SEQ ID NO:1, wherein said protein forms a complex with an ATP-binding site ligand, wherein the protein crystal has a crystal lattice in a P3<sub>2</sub>1 space group and unit cell dimensions, +/- 5%, of a = 72.12Å, b = 72.12 Å and c = 241.62 Å; and  
forming a crystalline form of the protein in the crystallization volume storing the crystallization volume under conditions suitable for crystal formation of the protein.
37. (Previously Presented) An isolated non-crystalline protein consisting of residues 596-900 of SEQ ID NO:1.
38. (Currently Amended) A non-crystalline protein ~~e~~onists consisting of SEQ ID NO:3.